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Myriad Genetics, Inc.

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<151> 1998-11-06

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Figure 1 consists of 12 histograms arranged horizontally, labeled x_1 through x_{12} . Each histogram shows the frequency of values for x_k ranging from 0 to 10. The y-axis for each histogram is labeled 'count' and ranges from 0 to 10. The distributions are roughly bell-shaped and centered around 5. The peak count increases from 10 for x_1 to 10 for x_{12} .

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 tgctagtggg tagaggtcag 20

21

37

38

2.1

19

38

39

37


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<400> 161
cacttgatgg gcgttctgag

20

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<213> Homo sapiens
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<400> 162
ttctgtcctt cagccaatgc

20

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<210> 163
<211> 38
<212> DNA
<213> Homo sapiens
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3.8

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38

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<400> 165
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19

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 <213> Homo sapiens

<400> 172
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<210> 173
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<400> 173
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<400> 182
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 <212> DNA
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<400> 185
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<210> 186
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<400> 186
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<210> 187
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<400> 187
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<400> 191
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<210> 193
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<400> 193
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<210> 194
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23

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<211> 24
<212> DNA
<213> Homo sapiens
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<400> 197
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24

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<212> DNA
<213> Homo sapiens
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<400> 198
gaggcttggg stccacata ag

22

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<213> Homo sapiens
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<400> 199
cctggcacag cygcgggcca gga

23

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<213> Homo sapiens
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23

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<400> 201
taaatgtttt ytcattctta g

21

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<400> 202
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<210> 203
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 <212> DNA
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<400> 203
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<210> 204
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 <212> DNA
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<400> 204
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<210> 205
 <211> 23
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<400> 205
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<210> 206
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<400> 206
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<210> 207
 <211> 23
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 <213> Homo sapiens

<400> 207
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<210> 208
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 208
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23

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<400> 210
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Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met Ser Gln
5 10 15

gga cgc acc ata tcg cag gca ccc gcc cgc cgc gag cgg ccg cgc aag 152
Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro Arg Lys
20 25 30

gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg tcg ggg 200
Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro Ser Gly
35 40 45 50

tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca gcg ggt 248
Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala Ala Gly
55 60 65

agc cgg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc aac 293
Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe Asn
70 75 80

cggtcagtea acgagccacg ccccgteccg ctggggccctc agtgcggcgc agcctct 350

<400> 211
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1 5 10 15

Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
20 25 30

Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
35 40 45

Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
50 55 60

Asn

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<222> (51) .. (269)
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<210> 213
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<213> Mus musculus

<400> 213
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  1                               5                               10                               15
Ser Gln Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg
                               20                               25                               30
His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn
                               35                               40                               45
Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala
  50                               55                               60
Ala Leu Tyr Val Phe Ser Glu Tyr Asn
  65                               70

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<210> 214
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Histidine
 containing motif.

<220>
 <221> SITE
 <222> (1)..(3)
 <223> These amino acids can each be any large
 hydrophobic residue.

<220>
 <221> SITE
 <222> (4)
 <223> This is serine or threonine.

<220>
 <221> SITE
 <222> (6)
 <223> This can be any amino acid residue.

<220>
 <221> SITE
 <222> (8)
 <223> This can be any amino acid residue.

<220>
 <221> SITE
 <222> (11)..(12)
 <223> These can be any amino acid residues.

<400> 214
 Xaa Xaa Xaa Xaa His Xaa His Xaa Asp His Xaa Xaa Gly
 1 5 10

<210> 215
 <211> 127
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(127)
 <223> Exon 1.

<400> 215
 tttaatacga ctactatag ggaatttggc cctcgagnng aattcggcac gagggtagcc 60
 ccgcgacagc tgggccgagg gtgcgggcct gcgctccctc ggctcctggc gcgggctcgg 120
 ggagagg 127

<210> 216
 <211> 983
 <212> DNA
 <213> Homo sapiens

Feature 2988550

<220>
 <221> intron
 <222> (1)..(300)
 <223> Upstream intron of exon 2.

<220>
 <221> misc_structure
 <222> (301)..(465)
 <223> Exon 2.

<220>
 <221> intron
 <222> (466)..(983)
 <223> Intron downstream of exon 2.

<400> 216
 gtctccatag ttttgccctt ttgagaacat catatagtta gaattcagct atagttttta 60
 attgcctggg tttggttatt tttgtttgtt tgggtgtgtg aacaattata caagatttgt 120
 taacttgtag ttttagccaa gttattaaaa cttactgtg gatatgtgtg gaatactatg 180
 agagaccaag aatccagact gttctaaata accaaaaagt aataatagag ataaatatta 240
 caggaatatg tttttggtcc agtgatatga aataatcccc agatgatctt tctgttgacg 300
 ggtggaagat gtctatggat gtgacattcc tggggacggg tgcagcatac ccatctccaa 360
 cccgggggtgc ctctgctgtg gtccctcggt gtgaaggcga gtgctggctc tttgactgtg 420
 gggaggggaac acagacacag cttatgaaaa gccaaactta agcagggttag tgtgccttca 480
 gctatctcat taagaatttt ttgttgttct gcttcatttt cttggctctc cttggacatt 540
 ttgttttagaa acagccctga tggttgcac ccacttcagt gctacaccct ggtgagactt 600
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 tcatttatcc tgtagatgct gaaagcaagg attcatgtag gcttgggggt tgggaaatgt 720
 cgtgggatac accaggcata ttagatgaac actgccttag caaggaagca gtgtacatac 780
 ttacctccac caggagatag ttttcatgag aggatgcaaa gggtaggaaa tgtttggagg 840
 aggagatgtt gttttcctct tggggttatc aggtaaactt ctacagagaag ttgacctgtg 900
 gattgtcaaa gagagagatt tcaggctgag agaagaaggc atttcatcag gggatggagt 960
 gagcagagcc acacctggga gat 983

<210> 217
 <211> 1287
 <212> DNA
 <213> Homo sapiens

<220>
 <221> intron
 <222> (1)..(300)
 <223> Intron upstream of exon 3.

<220>
 <221> misc_feature
 <222> (301)..(768)
 <223> Exon 3.

<220>
 <221> intron
 <222> (769)..(1287)
 <223> Intron downstream of exon 3.

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 aaaaaaaaaa aaactattaa aaacaaacaa acaaaaaaac acctggtgaa ataaagcctg 120
 tcttcttgtt tttggaatca tgtagcaaaa tgtaaataaa taagtttatg atgataagta 180
 gaacttttaa attcaattta ctatttttaa tgtaaattgt taggcttgtt tcaaatagct 240
 ttgtatgggt ttttagttaa tgaaaaattt ccaaacgtat ttctctatct caatcaaaag 300
 ggagaattac caagatcttc atcacacacc ttcattggaga ccatttcttt ggccttcctg 360
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 tctatggccc tgtagggctt cgggacttta tctggcgaac catggaactc tctcacacgg 480
 agctggtctt ccattatgtg gttcatgaac tggttcctac agcagatcaa tgtcctgcag 540
 aagaactaaa agaatttgcg catgtgaata gagcagacag tcctcccaaa gaggaacaag 600
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 ttgttgtaaa agcatttcgc ctctttcaca gaattccctc atttgggttt tcagtcgtgg 720
 aaaagaaacg ccaggtaaa ctcaatgoac agaaacttaa agaccttggg aagtgttttt 780
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 aaaaaaaagt gtcatagtaa gcttcactc ctctatccca ggcctgaaac tgacaatttc 1200
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 <212> DNA
 <213> Homo sapiens

<210> 219
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<220>
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<400> 219

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ccgcgacagc tgggccgagg gtgcgggcct gcgcctcctc ggctcctggc gcgggctcgg 120

ggagaggggt ggaag atg tct atg gat gtg aca ttc ctg ggg acg ggt gca 171
 Met Ser Met Asp Val Thr Phe Leu Gly Thr Gly Ala
 1 5 10

gca tac cca tct cca acc cgg ggt gcc tct gct gtg gtc ctt cgg tgt 219
 Ala Tyr Pro Ser Pro Thr Arg Gly Ala Ser Ala Val Val Leu Arg Cys
 15 20 25

gaa ggc gag tgc tgg ctc ttt gac tgt ggg gag gga aca cag aca cag 267
 Glu Gly Glu Cys Trp Leu Phe Asp Cys Gly Glu Gly Thr Gln Thr Gln
 30 35 40

ctt atg aaa agc caa ctt aaa gca ggg aga att acc aag atc ttc atc 315
 Leu Met Lys Ser Gln Leu Lys Ala Gly Arg Ile Thr Lys Ile Phe Ile
 45 50 55 60

aca cac ctt cat gga gac cat ttc ttt ggc ctt cct ggg ctc ctc tgc 363
 Thr His Leu His Gly Asp His Phe Phe Gly Leu Pro Gly Leu Leu Cys
 65 70 75

aca atc agc ctg cag agt ggc tcc atg gtg tcc aaa cag cct att gaa 411
 Thr Ile Ser Leu Gln Ser Gly Ser Met Val Ser Lys Gln Pro Ile Glu
 80 85 90

atc tat ggc cct gta ggg ctt cgg gac ttt atc tgg cga acc atg gaa 459
 Ile Tyr Gly Pro Val Gly Leu Arg Asp Phe Ile Trp Arg Thr Met Glu
 95 100 105

ctc tct cac acg gag ctg gtc ttc cat tat gtg gtt cat gaa ctg gtt 507
 Leu Ser His Thr Glu Leu Val Phe His Tyr Val Val His Glu Leu Val
 110 115 120

cct aca gca gat caa tgt cct gca gaa gaa cta aaa gaa ttt gcg cat 555
 Pro Thr Ala Asp Gln Cys Pro Ala Glu Glu Leu Lys Glu Phe Ala His
 125 130 135 140

gtg aat aga gca gac agt cct ccc aaa gag gaa caa gga aga act atc 603
 Val Asn Arg Ala Asp Ser Pro Pro Lys Glu Glu Gln Gly Arg Thr Ile
 145 150 155

ctg tta gac tca gaa gaa aac tca tac ctt ctg ttt gat gat gaa caa 651
 Leu Leu Asp Ser Glu Glu Asn Ser Tyr Leu Leu Phe Asp Asp Glu Gln
 160 165 170

ttt gtt gta aaa gca ttt cgc ctc ttt cac aga att ccc tca ttt ggg 699
 Phe Val Val Lys Ala Phe Arg Leu Phe His Arg Ile Pro Ser Phe Gly
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TC03T = 28988660

Asp Phe Met Val Ile Ser Ile Pro Ile Lys Lys
 355 360

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 <213> Mus musculus

<220>
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<400> 221

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1 5 10 15	
tcg cag ggt tgc gct cgt cgg ccg cgg cca ccc aaa gac cca ctg cga	96
Ser Gln Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg	
20 25 30	
cac ctg cgt acg cgg gag aag cgc ggc ccg ggt ccc ggg ggc ccg aac	144
His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn	
35 40 45	
acc gtg tac ctg cag gtg gtg gcg gcg ggc ggc cgg gac gcg ggg gct	192
Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala	
50 55 60	
gct ctc tat gtc ttc tgc gaa tac aac agg tac ctt ttt aac tgc gga	240
Ala Leu Tyr Val Phe Ser Glu Tyr Asn Arg Tyr Leu Phe Asn Cys Gly	
65 70 75 80	
gaa ggc gtc caa cga ctt atg cag gaa cac aag act gaa agt cgc tcg	288
Glu Gly Val Gln Arg Leu Met Gln Glu His Lys Thr Glu Ser Arg Ser	
85 90 95	
ctt gac aac atc ttt ctg act cgg atg cat tgg tca aat gtt ggg ggg	336
Leu Asp Asn Ile Phe Leu Thr Arg Met His Trp Ser Asn Val Gly Gly	
100 105 110	
ttg tgt gga atg att tta act tta aag gaa acc ggg ctt ccc aaa tgt	384
Leu Cys Gly Met Ile Leu Thr Leu Lys Glu Thr Gly Leu Pro Lys Cys	
115 120 125	
gtt ctg tct gga cca cca cag ctg gag aaa tat cta gaa gca atc aaa	432
Val Leu Ser Gly Pro Pro Gln Leu Glu Lys Tyr Leu Glu Ala Ile Lys	
130 135 140	
ata ttt tct ggt cca ttg aaa gga ata gaa ctg gcc gtg cgg cct cac	480
Ile Phe Ser Gly Pro Leu Lys Gly Ile Glu Leu Ala Val Arg Pro His	
145 150 155 160	
tct gca cca gaa tac aag gat gag acc atg act gtt tac cag gtc cct	528
Ser Ala Pro Glu Tyr Lys Asp Glu Thr Met Thr Val Tyr Gln Val Pro	
165 170 175	
atc cac agt gaa cgg agg tgt gga aag caa cag cca tcc cag agc ccc	576
Ile His Ser Glu Arg Arg Cys Gly Lys Gln Gln Pro Ser Gln Ser Pro	
180 185 190	

aga Arg	aca Thr	tct Ser 195	ccc Pro	aac Asn	agg Arg	ctc Leu	agt Ser 200	ccc Pro	aaa Lys	cag Gln	tca Ser	tcg Ser 205	gac Asp	tct Ser	gga Gly	624
tca Ser	gct Ala 210	gaa Glu	aat Asn	ggg Gly	cag Gln	tgc Cys 215	caa Gln	cag Gln	gaa Glu	agc Ser	atg Met 220	ggg Gly	cag Gln	gga Gly	ccc Pro	672
tcc Ser 225	tta Leu	gtg Val	gta Val	gct Ala	ttt Phe 230	gtc Val	tgc Cys	aag Lys	ctt Leu	cac His 235	ttg Leu	agg Arg	aaa Lys	gga Gly	aac Asn 240	720
ttc Phe	ttg Leu	gtg Val	ctt Leu	aaa Lys 245	gca Ala	aag Lys	gag Glu	ctg Leu	ggc Gly 250	ctt Leu	cct Pro	gtt Val	ggg Gly	acg Thr 255	gcc Ala	768
gcc Ala	att Ile	gca Ala 260	ccc Pro	atc Ile	att Ile	gct Ala	gct Ala 265	gtc Val	aag Lys	gac Asp	ggg Gly	aag Lys 270	agt Ser	atc Ile	act Thr	816
tac Tyr	gaa Glu 275	gga Gly	aga Arg	gag Glu	att Ile	gct Ala	gct Ala 280	gaa Glu	gag Glu	ctt Leu	tgt Cys	aca Thr 285	ccc Pro	cca Pro	gat Asp	864
cct Pro 290	ggt Gly	ctt Leu	gta Val	ttc Phe	atc Ile	gtg Val 295	gta Val	gag Glu	tgt Cys	cct Pro	gat Asp 300	gaa Glu	gga Gly	ttc Phe	atc Ile	912
ctg Leu 305	ccc Pro	atc Ile	tgt Cys	gag Glu	aac Asn 310	gac Asp	acc Thr	ttt Phe	aaa Lys	agg Arg 315	tac Tyr	cag Gln	gca Ala	gag Glu	gct Ala 320	960
gat Asp	gca Ala	cct Pro	gtg Val	gcg Ala 325	ctg Leu	gtg Val	gtc Val	cac His	ata Ile 330	gcc Ala	cca Pro	gaa Glu	tct Ser	gta Val 335	ctc Leu	1008
atc Ile	gac Asp	agc Ser	aga Arg 340	tac Tyr	cag Gln	cag Gln	tgg Trp	atg Met 345	gag Glu	agg Arg	ttc Phe	ggg Gly	cct Pro 350	gac Asp	aca Thr	1056
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ccc Pro 385	cag Gln	ctt Leu	acc Thr	agc Ser	ttc Phe 390	tat Tyr	agt Ser	aag Lys	gag Glu	gaa Glu 395	ggg Gly	tcc Ser	acc Thr	ctc Leu	agc Ser 400	1200
gtg Val	cca Pro	aca Thr	gtt Val	cgg Arg 405	ggg Gly	gaa Glu	tgc Cys	ctc Leu	ctc Leu 410	aag Lys	tat Tyr	tca Ser	gtc Val	cgc Arg 415	ccc Pro	1248
aag Lys	aga Arg	gag Glu	tgg Trp 420	cag Gln	agg Arg	gat Asp	acc Thr	aca Thr 425	ctc Leu	gac Asp	tgc Cys	aat Asn 430	act Thr	gat Asp	gaa Glu	1296
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gag Glu	tat Tyr 450	cgg Arg	aag Lys	aac Asn	gtg Val	cag Gln 455	gaa Glu	aac Asn	cca Pro	gcc Ala 460	cca Pro	gca Ala	gag Glu	aaa Lys	aga Arg	1392
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atg Met	gag Glu	atc Ile	cga Arg	aat Asn 485	gtc Val	agt Ser	tcc Ser	aca Thr	ctc Leu 490	gtc Val	aac Asn	cta Leu	agc Ser	cct Pro 495	gac Asp	1488
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cgt Arg	cat His	tac Tyr 515	gga Gly	cag Gln	caa Gln	ata Ile	gac Asp 520	cga Arg	gtc Val	tta Leu	tgc Cys	agc Ser 525	ctc Leu	acg Thr	gct Ala	1584
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cag Gln 625	acc Thr	tgc Cys	ctg Leu	gta Val	cgg Arg 630	cac His	tgc Cys	aag Lys	cat His	gct Ala 635	ttt Phe	ggc Gly	tgt Cys	gca Ala	ctg Leu 640	1920
gta Val	cat His	tca Ser	tct Ser	ggc Gly 645	tgg Trp	aaa Lys	gtc Val	gtc Val	tac Tyr 650	tcg Ser	ggg Gly	gat Asp	acc Thr	atg Met 655	ccc Pro	1968
tgt Cys	gag Glu	gct Ala	ctg Leu 660	gtc Val	cag Gln	atg Met	ggg Gly 665	aaa Lys 665	gat Asp	gcc Ala	acc Thr	ctc Leu	ctg Leu 670	ata Ile	cat His	2016
gaa Glu	gcc Ala	act Thr 675	ctg Leu	gag Glu	gat Asp	cnc Xaa 680	ttg Leu 680	gaa Glu	gag Glu	gaa Glu	gca Ala	gta Val 685	gag Glu	agg Arg	aca Thr	2064
cac His	agc Ser 690	acc Thr	acc Thr	tcc Ser	cag Gln	gct Ala 695	att Ile	aat Asn	gtg Val	ggg Gly 700	atg Met	cgg Arg	atg Met	aat Asn	gcg Ala	2112

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 Glu Phe Ile Met Leu Asn His Phe Ser Gln Arg Tyr Xaa Lys Ile Pro
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 Met Lys Val Xaa Phe Gly Asp Phe Pro Thr Val Pro Lys Leu Ile Pro
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Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala
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Ala Leu Tyr Val Phe Ser Glu Tyr Asn Arg Tyr Leu Phe Asn Cys Gly
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Glu Gly Val Gln Arg Leu Met Gln Glu His Lys Thr Glu Ser Arg Ser
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Leu Asp Asn Ile Phe Leu Thr Arg Met His Trp Ser Asn Val Gly Gly
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Leu Cys Gly Met Ile Leu Thr Leu Lys Glu Thr Gly Leu Pro Lys Cys
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 Pro Gln Leu Thr Ser Phe Tyr Ser Lys Glu Glu Gly Ser Thr Leu Ser
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 Lys Arg Glu Trp Gln Arg Asp Thr Thr Leu Asp Cys Asn Thr Asp Glu
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 Glu Tyr Arg Lys Asn Val Gln Glu Asn Pro Ala Pro Ala Glu Lys Arg
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 Arg His Tyr Gly Gln Gln Ile Asp Arg Val Leu Cys Ser Leu Thr Ala
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 Val Phe Val Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn
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 Gln Tyr His Asn His Cys Gln Glu Ile Leu His His Val Ser Met Ile
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 Pro Ala Lys Cys Leu Gln Lys Gly Ala Glu Val Ser Asn Thr Thr Leu
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 Val His Ser Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro
 645 650 655
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 Glu Ala Thr Leu Glu Asp Xaa Leu Glu Glu Glu Ala Val Glu Arg Thr
 675 680 685
 His Ser Thr Thr Ser Gln Ala Ile Asn Val Gly Met Arg Met Asn Ala
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 Leu Phe Ser Pro Asp Phe Asn Glu Lys Val Gly Ile Ala Phe Asp His
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Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Ile Gln Arg Leu Met Gln	
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Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu	
115 120 125	
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Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu	
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Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly	
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Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu	
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Pro	Glu	Arg	Ser	Ser	Asp	Ser	Glu	Ser	Asn	Glu	Asn	Glu	Pro	His	Leu	
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Pro	His	Gly	Val	Ser	Gln	Arg	Arg	Gly	Val	Arg	Asp	Ser	Ser	Leu	Val	
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Leu	Lys	Ala	Lys	Glu	Met	Gly	Leu	Pro	Val	Gly	Thr	Ala	Ala	Ile	Ala	
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ccc	atc	att	gct	gct	gtc	aag	gac	ggg	aaa	agc	atc	act	cat	gaa	gga	864
Pro	Ile	Ile	Ala	Ala	Val	Lys	Asp	Gly	Lys	Ser	Ile	Thr	His	Glu	Gly	
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Ala	Phe	Val	Val	Val	Glu	Cys	Pro	Asp	Glu	Ser	Phe	Ile	Gln	Pro	Ile	
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Cys	Glu	Asn	Ala	Thr	Phe	Gln	Arg	Tyr	Gln	Gly	Lys	Ala	Asp	Ala	Pro	
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Val	Ala	Leu	Val	Val	His	Met	Ala	Pro	Glu	Ser	Val	Leu	Val	Asp	Ser	
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Arg	Tyr	Gln	Gln	Trp	Met	Glu	Arg	Phe	Gly	Pro	Asp	Thr	Gln	His	Leu	
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gtc	ctg	aat	gag	aac	tgt	gcc	tca	gtt	cac	aac	ctt	cgc	agc	cac	aag	1152
Val	Leu	Asn	Glu	Asn	Cys	Ala	Ser	Val	His	Asn	Leu	Arg	Ser	His	Lys	
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Ile	Gln	Thr	Gln	Leu	Asn	Leu	Ile	His	Pro	Asp	Ile	Phe	Pro	Leu	Leu	
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acc	agt	ttc	ccc	tgt	aag	aag	gag	ggc	ccc	acc	ctc	agt	gtg	ccc	atg	1248
Thr	Ser	Phe	Pro	Cys	Lys	Lys	Glu	Gly	Pro	Thr	Leu	Ser	Val	Pro	Met	
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Val	Gln	Gly	Glu	Cys	Leu	Leu	Lys	Tyr	Gln	Leu	Arg	Pro	Arg	Arg	Glu	
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Trp	Gln	Arg	Asp	Ala	Ile	Ile	Thr	Cys	Asn	Pro	Glu	Glu	Phe	Ile	Ile	
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Ser	Gly	Trp	Lys 660	Val	Val	Tyr	Ser	Gly 665	Asp	Thr	Met	Pro	Cys 670	Glu	Ala
Leu	Val	Arg 675	Met	Gly	Lys	Asp	Ala 680	Thr	Leu	Leu	Ile	His 685	Glu	Ala	Thr
Leu	Glu 690	Asp	Gly	Leu	Glu	Glu 695	Glu	Ala	Val	Glu	Lys 700	Thr	His	Ser	Thr
Thr 705	Ser	Gln	Ala	Ile	Ser 710	Val	Gly	Met	Arg	Met 715	Asn	Ala	Glu	Phe	Ile 720

aag Lys	gaa Glu 130	acc Thr	ggg Gly	ctt Leu	cca Pro	aag Lys 135	tgt Cys	gta Val	ctt Leu	tct Ser	gga Gly 140	cct Pro	cca Pro	cag Gln	ctg Leu	432
gaa Glu 145	aaa Lys	tac Tyr	ctc Leu	gaa Glu	gca Ala 150	atc Ile	aaa Lys	ata Ile	ttt Phe	tct Ser 155	ggt Gly	cca Pro	ttg Leu	aaa Lys	gga Gly 160	480
ata Ile	gaa Glu	ctg Leu	gct Ala	gtg Val 165	cgg Arg	ccc Pro	cac His	tct Ser	gcc Ala 170	cca Pro	gaa Glu	tac Tyr	gag Glu	gat Asp 175	gaa Glu	528
acc Thr	atg Met	aca Thr	gtt Val 180	tac Tyr	cag Gln	atc Ile	ccc Pro	ata Ile 185	cac His	agt Ser	gaa Glu	cag Gln	agg Arg 190	agg Arg	gga Gly	576
agg Arg	cac His	caa Gln 195	cca Pro	tgg Trp	cag Gln	agt Ser	cca Pro 200	gaa Glu	agg Arg	cct Pro	ctc Leu	agc Ser 205	agg Arg	ctc Leu	agt Ser	624
cca Pro	gag Glu 210	cga Arg	tct Ser	tca Ser	gac Asp	tcc Ser 215	gag Glu	tcg Ser	aat Asn	gaa Glu	aat Asn 220	gag Glu	cca Pro	cac His	ctt Leu	672
cca Pro 225	cat His	ggt Gly	gtt Val	agc Ser	cag Gln 230	aga Arg	aga Arg	ggg Gly	gtc Val	agg Arg 235	gac Asp	tct Ser	tcc Ser	ctg Leu	gtc Val 240	720
gta Val	gct Ala	ttc Phe	atc Ile	tgt Cys 245	aag Lys	ctt Leu	cac His	tta Leu	aag Lys 250	aga Arg	gga Gly	aac Asn	ttc Phe	ttg Leu 255	gtg Val	768
ctc Leu	aaa Lys	gca Ala	aag Lys 260	gag Glu	atg Met	ggc Gly	ctc Leu	cca Pro 265	gtt Val	ggg Gly	aca Thr	gct Ala	gcc Ala 270	atc Ile	gct Ala	816
ccc Pro	atc Ile	att Ile 275	gct Ala	gct Ala	gtc Val	aag Lys	gac Asp 280	ggg Gly	aaa Lys	agc Ser	atc Ile	act Thr 285	cat His	gaa Glu	gga Gly	864
aga Arg	gag Glu 290	att Ile	ttg Leu	gct Ala	gaa Glu	gag Glu 295	ctg Leu	tgt Cys	act Thr	cct Pro	cca Pro 300	gat Asp	cct Pro	ggg Gly	gct Ala	912
gct Ala 305	ttt Phe	gtg Val	gtg Val	gta Val	gaa Glu 310	tgt Cys	cca Pro	gat Asp	gaa Glu	agc Ser 315	ttc Phe	att Ile	caa Gln	ccc Pro	atc Ile 320	960
tgt Cys	gag Glu	aat Asn	gcc Ala	acc Thr 325	ttt Phe	cag Gln	agg Arg	tac Tyr	caa Gln 330	gga Gly	aag Lys	gca Ala	gat Asp	gcc Ala 335	ccc Pro	1008
gtg Val	gcc Ala	ttg Leu	gtg Val	gtt Val	cac His	atg Met	gcc Ala	cca Pro 345	gaa Glu	tct Ser	gtg Val	ctt Leu	gtg Val 350	gac Asp	agc Ser	1056
agg Arg	tac Tyr	cag Gln 355	cag Gln	tgg Trp	atg Met	gag Glu	agg Arg 360	ttt Phe	ggg Gly	cct Pro	gac Asp	acc Thr 365	cag Gln	cac His	ttg Leu	1104
gtc Val	ctg Leu 370	aat Asn	gag Glu	aac Asn	tgt Cys	gcc Ala 375	tca Ser	gtt Val	cac His	aac Asn 380	ctt Leu	cgc Arg	agc Ser	cac His	aag Lys	1152

att	caa	acc	cag	ctc	aac	ctc	atc	cac	ccg	gac	atc	ttc	ccc	ctg	ctc	1200
Ile	Gln	Thr	Gln	Leu	Asn	Leu	Ile	His	Pro	Asp	Ile	Phe	Pro	Leu	Leu	
385					390					395					400	
acc	agt	ttc	ccc	tgt	aag	aag	gag	ggc	ccc	acc	ctc	agt	gtg	ccc	atg	1248
Thr	Ser	Phe	Pro	Cys	Lys	Lys	Glu	Gly	Pro	Thr	Leu	Ser	Val	Pro	Met	
				405					410					415		
gtt	cag	ggc	gaa	tgc	ctc	ctc	aag	tac	cag	ctc	cgt	ccc	agg	agg	gaa	1296
Val	Gln	Gly	Glu	Cys	Leu	Leu	Lys	Tyr	Gln	Leu	Arg	Pro	Arg	Arg	Glu	
			420					425					430			
tgg	cag	agg	gat	gcc	att	atc	act	tgc	aat	cct	gag	gaa	ttc	ata	gtt	1344
Trp	Gln	Arg	Asp	Ala	Ile	Ile	Thr	Cys	Asn	Pro	Glu	Glu	Phe	Ile	Val	
			435				440						445			
gag	gcg	ctg	cag	ctt	ccc	aac	ttc	cag	cag	agt	gtg	cag	gag	tac	agg	1392
Glu	Ala	Leu	Gln	Leu	Pro	Asn	Phe	Gln	Gln	Ser	Val	Gln	Glu	Tyr	Arg	
	450					455					460					
agg	agt	gtg	cag	gac	gtc	cca	gcc	cca	gca	gag	aaa	aga	agt	cag	tac	1440
Arg	Ser	Val	Gln	Asp	Val	Pro	Ala	Pro	Ala	Glu	Lys	Arg	Ser	Gln	Tyr	
465					470					475					480	
cca	gaa	atc	atc	ttc	ctt	gga	aca	ggg	tct	gcc	atc	ccc	atg	aag	att	1488
Pro	Glu	Ile	Ile	Phe	Leu	Gly	Thr	Gly	Ser	Ala	Ile	Pro	Met	Lys	Ile	
				485					490					495		
cga	aat	gtc	agt	gcc	aca	ctt	gtc	aac	ata	agc	ccc	gac	acg	tct	ctg	1536
Arg	Asn	Val	Ser	Ala	Thr	Leu	Val	Asn	Ile	Ser	Pro	Asp	Thr	Ser	Leu	
				500				505					510			
cta	ctg	gac	tgt	ggc	gag	ggc	acg	ttt	ggg	cag	ctg	tgc	cgt	cat	tac	1584
Leu	Leu	Asp	Cys	Gly	Glu	Gly	Thr	Phe	Gly	Gln	Leu	Cys	Arg	His	Tyr	
		515					520					525				
gga	gac	cag	gtg	gac	agg	gtc	ctg	ggc	acc	ctg	gct	gct	gtg	ttt	gtg	1632
Gly	Asp	Gln	Val	Asp	Arg	Val	Leu	Gly	Thr	Leu	Ala	Ala	Val	Phe	Val	
	530					535					540					
tcc	cac	ctg	cac	gca	gat	cac	cac	acg	ggc	ttg	cta	aat	atc	ttg	ctg	1680
Ser	His	Leu	His	Ala	Asp	His	His	Thr	Gly	Leu	Leu	Asn	Ile	Leu	Leu	
545					550				555						560	
cag	aga	gaa	caa	gcc	ttg	gca	tct	ttg	gga	aag	ccc	ctt	cac	cct	ttg	1728
Gln	Arg	Glu	Gln	Ala	Leu	Ala	Ser	Leu	Gly	Lys	Pro	Leu	His	Pro	Leu	
				565					570					575		
ctg	gtg	gtt	gcc	ccc	agc	cag	ctc	aaa	gcc	tgg	ctc	cag	cag	tac	cac	1776
Leu	Val	Val	Ala	Pro	Ser	Gln	Leu	Lys	Ala	Trp	Leu	Gln	Gln	Tyr	His	
			580					585					590			
aac	cag	tgc	cag	gag	gtc	ctg	cac	cac	atc	agt	atg	att	cct	gcc	aaa	1824
Asn	Gln	Cys	Gln	Glu	Val	Leu	His	His	Ile	Ser	Met	Ile	Pro	Ala	Lys	
		595					600					605				
tgc	ctt	cag	gaa	ggg	gct	gag	atc	tcc	agt	cct	gca	gtg	gaa	aga	ttg	1872
Cys	Leu	Gln	Glu	Gly	Ala	Glu	Ile	Ser	Ser	Pro	Ala	Val	Glu	Arg	Leu	
	610					615					620					
atc	agt	tgc	ctg	ttg	cga	aca	tgt	gat	ttg	gaa	gag	ttt	cag	acc	tgt	1920
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 <212> PRT
 <213> Gorilla gorilla

<400> 226

Met Trp Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met
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 20 25 30
 Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
 35 40 45
 Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
 50 55 60
 Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
 65 70 75 80
 Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
 85 90 95
 Glu His Lys Leu Lys Val Val Arg Leu Asp Asn Ile Phe Leu Thr Arg
 100 105 110
 Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
 115 120 125
 Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
 130 135 140
 Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
 145 150 155 160
 Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
 165 170 175
 Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
 180 185 190
 Arg His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
 195 200 205
 Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
 210 215 220
 Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
 225 230 235 240
 Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
 245 250 255
 Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
 260 265 270
 Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
 275 280 285
 Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
 290 295 300

TOO2T 2898660

Ala 305	Phe	Val	Val	Val	Glu 310	Cys	Pro	Asp	Glu	Ser 315	Phe	Ile	Gln	Pro	Ile 320
Cys	Glu	Asn	Ala	Thr 325	Phe	Gln	Arg	Tyr	Gln 330	Gly	Lys	Ala	Asp	Ala 335	Pro
Val	Ala	Leu	Val	Val	His	Met	Ala	Pro 345	Glu	Ser	Val	Leu	Val	Asp 350	Ser
Arg	Tyr	Gln 355	Gln	Trp	Met	Glu	Arg 360	Phe	Gly	Pro	Asp	Thr 365	Gln	His	Leu
Val	Leu 370	Asn	Glu	Asn	Cys	Ala 375	Ser	Val	His	Asn	Leu 380	Arg	Ser	His	Lys
Ile 385	Gln	Thr	Gln	Leu	Asn 390	Leu	Ile	His	Pro	Asp 395	Ile	Phe	Pro	Leu	Leu 400
Thr	Ser	Phe	Pro	Cys 405	Lys	Lys	Glu	Gly	Pro 410	Thr	Leu	Ser	Val	Pro 415	Met
Val	Gln	Gly	Glu 420	Cys	Leu	Leu	Lys	Tyr 425	Gln	Leu	Arg	Pro	Arg 430	Arg	Glu
Trp	Gln	Arg 435	Asp	Ala	Ile	Ile	Thr 440	Cys	Asn	Pro	Glu	Glu 445	Phe	Ile	Val
Glu	Ala 450	Leu	Gln	Leu	Pro	Asn 455	Phe	Gln	Gln	Ser	Val 460	Gln	Glu	Tyr	Arg
Arg 465	Ser	Val	Gln	Asp	Val 470	Pro	Ala	Pro	Ala	Glu 475	Lys	Arg	Ser	Gln	Tyr 480
Pro	Glu	Ile	Ile	Phe 485	Leu	Gly	Thr	Gly	Ser 490	Ala	Ile	Pro	Met	Lys 495	Ile
Arg	Asn	Val	Ser 500	Ala	Thr	Leu	Val	Asn 505	Ile	Ser	Pro	Asp	Thr 510	Ser	Leu
Leu	Leu	Asp 515	Cys	Gly	Glu	Gly	Thr 520	Phe	Gly	Gln	Leu	Cys 525	Arg	His	Tyr
Gly	Asp 530	Gln	Val	Asp	Arg	Val 535	Leu	Gly	Thr	Leu	Ala 540	Ala	Val	Phe	Val
Ser 545	His	Leu	His	Ala	Asp 550	His	His	Thr	Gly	Leu 555	Leu	Asn	Ile	Leu	Leu 560
Gln	Arg	Glu	Gln	Ala 565	Leu	Ala	Ser	Leu	Gly 570	Lys	Pro	Leu	His	Pro 575	Leu
Leu	Val	Val	Ala 580	Pro	Ser	Gln	Leu	Lys 585	Ala	Trp	Leu	Gln	Gln 590	Tyr	His
Asn	Gln	Cys 595	Gln	Glu	Val	Leu	His 600	His	Ile	Ser	Met	Ile 605	Pro	Ala	Lys
Cys	Leu 610	Gln	Glu	Gly	Ala	Glu 615	Ile	Ser	Ser	Pro	Ala 620	Val	Glu	Arg	Leu
Ile 625	Ser	Ser	Leu	Leu	Arg 630	Thr	Cys	Asp	Leu	Glu 635	Glu	Phe	Gln	Thr	Cys 640

Thr Pro Leu Lys Thr Tyr Met Phe Asn Cys Pro Glu Asn Ala Cys Arg
 115 120 125
 Phe Leu Trp Gln Leu Arg Ile Arg Ser Ser Ser Val Val Asp Leu Phe
 130 135 140
 Ile Thr Ser Ala Asn Trp Asp Asn Ile Ala Gly Ile Ser Ser Ile Leu
 145 150 155 160
 Leu Ser Lys Glu Ser Asn Ala Leu Ser Thr Arg Leu His Gly Ala Met
 165 170 175
 Asn Ile Lys His Phe Leu Glu Cys Ile Arg Pro Phe Gln Asp Ser Asp
 180 185 190
 Tyr Gly Ser Cys Lys Tyr Pro Ser Gln Val Glu Glu Arg Pro Tyr Thr
 195 200 205
 Met Glu Asn Tyr Glu Asp Ala Gly Leu Lys Val Thr Tyr Ile Pro Leu
 210 215 220
 Ser Pro Pro Leu Asn Ile Gly Ser Asn Asn Glu Lys Ser Lys Asn Val
 225 230 235 240
 Lys Val Asn Asn Val Asp Ile Ala Phe Leu Ile Glu Met Lys Glu Ala
 245 250 255
 Ala Arg Arg Ile Asp Thr Met Lys Leu Met Glu Leu Lys Val Pro Lys
 260 265 270
 Gly Pro Leu Ile Gly Lys Leu Lys Ser Gly Glu Ala Val Thr Leu Pro
 275 280 285
 Asp Gly Arg Thr Ile Gln Pro Asp Gln Val Phe Ser Ser Asp Lys Val
 290 295 300
 Glu Gly Asp Lys Pro Leu Leu Leu Val Thr Glu Cys Thr Thr Glu Asp
 305 310 315 320
 His Val Lys Ala Leu Ile Asp Ser Ser Ser Leu Gln Pro Phe Leu Asn
 325 330 335
 Gly Glu Lys Gln Leu Asp Tyr Met Val His Ile Ser Asp Asp Ala Val
 340 345 350
 Ile Asn Thr Pro Thr Tyr Arg His Leu Met Glu Lys Leu Asn Asn Pro
 355 360 365
 Ser Ile Thr His Leu Leu Ile Asn Gly Gly Asn Pro Val Ile Pro Ala
 370 375 380
 Val Glu Ser Val Tyr Lys His Thr Arg Leu Leu Arg Ser Ile Ala Pro
 385 390 395 400
 Ser Leu Phe Pro Ala Leu His Pro Ile Asp Trp Ser Gly Ile Ile Thr
 405 410 415
 Gln Asn Glu Glu Leu Ser Gln Arg Gln Asp Gln Phe Ile Arg Val Ala
 420 425 430
 Pro Met Gln Arg Tyr Trp Met Arg Arg Gly Ala Ser Phe Asn Glu Glu
 435 440 445

T00027 28988660

Glu Pro Val Ile Val Val Gly Pro Arg Pro Leu Lys Arg Phe Leu Asp
 580 585 590
 Ala Tyr Gln Arg Leu Glu Asp Leu Asp Met Glu Phe Leu Asp Cys Arg
 595 600 605
 Ser Thr Thr Ala Thr Ser Trp Ala Ser Leu Glu Ser Gly Gly Glu Ala
 610 615 620
 Glu Gly Ser Leu Phe Thr Gln Gly Ser Pro Met Gln Ser Val Phe Lys
 625 630 635 640
 Arg Ser Asp Ile Ser Met Asp Asn Ser Ser Val Leu Leu Cys Leu Lys
 645 650 655
 Asn Leu Lys Lys Val Leu Ser Glu Ile Gly Leu Asn Asp Leu Ile Ser
 660 665 670
 Phe Pro Val Val His Cys Pro Gln Ala Tyr Gly Val Val Ile Lys Ala
 675 680 685
 Ala Glu Arg Val Asn Ser Val Gly Glu Gln Ile Leu Gly Trp Lys Met
 690 695 700
 Val Tyr Ser Gly Asp Ser Arg Pro Cys Pro Glu Thr Val Glu Ala Ser
 705 710 715 720
 Arg Asp Ala Thr Ile Leu Ile His Glu Ala Thr Phe Glu Asp Ala Leu
 725 730 735
 Ile Glu Glu Ala Leu Ala Lys Asn His Ser Thr Thr Lys Glu Ala Ile
 740 745 750
 Asp Val Gly Ser Ala Ala Asn Val Tyr Arg Ile Val Leu Thr His Phe
 755 760 765
 Ser Gln Arg Tyr Pro Lys Ile Pro Val Ile Asp Glu Ser His Met His
 770 775 780
 Asn Thr Cys Ile Ala Phe Asp Leu Met Ser Ile Asn Met Ala Asp Leu
 785 790 795 800
 His Val Leu Pro Lys Val Leu Pro Tyr Phe Lys Thr Leu Phe Arg Asp
 805 810 815
 Glu Met Val Glu Asp Glu Asp Ala Asp Asp Val Ala Met Asp Asp Leu
 820 825 830
 Lys Glu Glu Ala Leu
 835

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 <212> PRT
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<400> 229
 Met Phe Thr Phe Ile Pro Ile Thr His Pro Thr Ser Asp Thr Lys His
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 Pro Leu Leu Leu Val Gln Ser Ala His Gly Glu Lys Tyr Phe Phe Gly
 20 25 30

T0022T 20000000

Lys Ile Gly Glu Gly Ser Gln Arg Ser Leu Thr Glu Asn Lys Ile Arg
 35 40 45
 Ile Ser Lys Leu Lys Asp Ile Phe Leu Thr Gly Glu Leu Asn Trp Ser
 50 55 60
 Asp Ile Gly Gly Leu Pro Gly Met Ile Leu Thr Ile Ala Asp Gln Gly
 65 70 75 80
 Lys Ser Asn Leu Val Leu His Tyr Gly Asn Asp Ile Leu Asn Tyr Ile
 85 90 95
 Val Ser Thr Trp Arg Tyr Phe Val Phe Arg Phe Gly Ile Asp Leu Asn
 100 105 110
 Asp His Ile Met Lys Asp Lys Glu Val Tyr Lys Asp Lys Ile Ile Ala
 115 120 125
 Val Lys Ser Phe Asn Val Leu Lys Asn Gly Gly Glu Asp Arg Leu Gly
 130 135 140
 Val Phe Asp Ser Phe Gln Lys Gly Val Leu Arg Ser Ile Val Ala Lys
 145 150 155 160
 Met Phe Pro Lys His Ala Pro Thr Asp Arg Tyr Asp Pro Ser Ser Asp
 165 170 175
 Pro His Leu Asn Val Glu Leu Pro Asp Leu Asp Ala Lys Val Glu Val
 180 185 190
 Ser Thr Asn Tyr Glu Ile Ser Phe Ser Pro Val Arg Gly Lys Phe Lys
 195 200 205
 Val Glu Glu Ala Ile Lys Leu Gly Val Pro Lys Gly Pro Leu Phe Ala
 210 215 220
 Lys Leu Thr Lys Gly Gln Thr Ile Thr Leu Asp Asn Gly Ile Val Val
 225 230 235 240
 Thr Pro Glu Gln Val Leu Glu Asn Glu Arg His Phe Ala Lys Val Leu
 245 250 255
 Ile Leu Asp Ile Pro Asp Asp Leu Tyr Leu Asn Ala Phe Val Glu Lys
 260 265 270
 Phe Lys Asp Tyr Asp Cys Ala Glu Leu Gly Met Val Tyr Tyr Phe Leu
 275 280 285
 Gly Asp Glu Val Thr Ile Asn Asp Asn Leu Phe Ala Phe Ile Asp Ile
 290 295 300
 Phe Glu Lys Asn Asn Tyr Gly Lys Val Asn His Met Ile Ser His Asn
 305 310 315 320
 Lys Ile Ser Pro Asn Thr Ile Ser Phe Phe Gly Ser Ala Leu Thr Thr
 325 330 335
 Leu Lys Leu Lys Ala Leu Gln Val Asn Asn Tyr Asn Leu Pro Lys Thr
 340 345 350
 Asp Arg Val Phe Ser Lys Asp Phe Tyr Asp Arg Phe Asp Thr Pro Leu
 355 360 365

0908067-11004
 T0002T-2000060

Ser	Arg	Gly	Thr	Ser	Met	Cys	Lys	Ser	Gln	Glu	Glu	Pro	Leu	Asn	Thr	
370						375					380					
Ile	Ile	Glu	Lys	Asp	Asn	Ile	His	Ile	Phe	Ser	Gln	Asn	Lys	Thr	Val	
385					390					395					400	
Thr	Phe	Glu	Pro	Phe	Arg	Met	Asn	Glu	Glu	Pro	Met	Lys	Cys	Asn	Ile	
				405					410					415		
Asn	Gly	Glu	Val	Ala	Asp	Phe	Ser	Trp	Gln	Glu	Ile	Phe	Glu	Glu	His	
			420					425					430			
Val	Lys	Pro	Leu	Glu	Phe	Pro	Leu	Ala	Asp	Val	Asp	Thr	Val	Ile	Asn	
		435					440					445				
Asn	Gln	Leu	His	Val	Asp	Asn	Phe	Asn	Asn	Ser	Ala	Glu	Lys	Lys	Lys	
	450					455					460					
His	Val	Glu	Ile	Ile	Thr	Leu	Gly	Thr	Gly	Ser	Ala	Leu	Pro	Ser	Lys	
465					470					475						480
Tyr	Arg	Asn	Val	Val	Ser	Thr	Leu	Val	Lys	Val	Pro	Phe	Thr	Asp	Ala	
				485					490					495		
Asp	Gly	Asn	Thr	Ile	Asn	Arg	Asn	Ile	Met	Leu	Asp	Ala	Gly	Glu	Asn	
			500					505					510			
Thr	Leu	Gly	Thr	Ile	His	Arg	Met	Phe	Ser	Gln	Leu	Ala	Val	Lys	Ser	
		515					520					525				
Ile	Phe	Gln	Asp	Leu	Lys	Met	Ile	Tyr	Leu	Ser	His	Leu	His	Ala	Asp	
	530					535					540					
His	His	Leu	Gly	Ile	Ile	Ser	Val	Leu	Asn	Glu	Trp	Tyr	Lys	Tyr	Asn	
545					550					555					560	
Lys	Asp	Asp	Glu	Thr	Ser	Tyr	Ile	Tyr	Val	Val	Thr	Pro	Trp	Gln	Tyr	
				565					570					575		
His	Lys	Phe	Val	Asn	Glu	Trp	Leu	Val	Leu	Glu	Asn	Lys	Glu	Ile	Leu	
			580					585					590			
Lys	Arg	Ile	Lys	Tyr	Ile	Ser	Cys	Glu	His	Phe	Ile	Asn	Asp	Ser	Phe	
	595						600					605				
Val	Arg	Met	Gln	Thr	Gln	Ser	Val	Pro	Leu	Ala	Glu	Phe	Asn	Glu	Ile	
	610					615					620					
Leu	Lys	Glu	Asn	Ser	Asn	Gln	Glu	Ser	Asn	Arg	Lys	Leu	Glu	Leu	Asp	
625					630					635					640	
Arg	Asp	Ser	Ser	Tyr	Arg	Asp	Val	Asp	Leu	Ile	Arg	Gln	Met	Tyr	Glu	
				645					650					655		
Asp	Leu	Ser	Ile	Glu	Tyr	Phe	Gln	Thr	Cys	Arg	Ala	Ile	His	Cys	Asp	
			660					665					670			
Trp	Ala	Tyr	Ser	Asn	Ser	Ile	Thr	Phe	Arg	Met	Asp	Glu	Asn	Asn	Glu	
		675					680					685				
His	Asn	Thr	Phe	Lys	Val	Ser	Tyr	Ser	Gly	Asp	Thr	Arg	Pro	Asn	Ile	
	690					695				700						

Glu Lys Phe Ser Leu Glu Ile Gly Tyr Asn Ser Asp Leu Leu Ile His
705 710 715 720

Glu Ala Thr Leu Glu Asn Gln Leu Leu Glu Asp Ala Val Lys Lys Lys
725 730 735

His Cys Thr Ile Asn Glu Ala Ile Gly Val Ser Asn Lys Met Asn Ala
740 745 750

Arg Lys Leu Ile Leu Thr His Phe Ser Gln Arg Tyr Pro Lys Leu Pro
755 760 765

Gln Leu Asp Asn Asn Ile Asp Val Met Ala Arg Glu Phe Cys Phe Ala
770 775 780

Phe Asp Ser Met Ile Val Asp Tyr Glu Lys Ile Gly Glu Gln Gln Arg
785 790 795 800

Ile Phe Pro Leu Leu Asn Lys Ala Phe Val Glu Glu Lys Glu Glu Glu
805 810 815

Glu Asp Val Asp Asp Val Glu Ser Val Gln Asp Leu Glu Val Lys Leu
820 825 830

Lys Lys His Lys Lys Asn
835

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<212> PRT

<213> Escherichia coli

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Gly Val Pro Thr Arg Thr Arg Asn Val Thr Ala Ile Leu Leu Asn Leu
20 25 30

Gln His Pro Thr Gln Ser Gly Leu Trp Leu Phe Asp Cys Gly Glu Gly
35 40 45

Thr Gln His Gln Leu Leu His Thr Ala Phe Asn Pro Gly Lys Leu Asp
50 55 60

Lys Ile Phe Ile Ser His Leu His Gly Asp His Leu Phe Gly Leu Pro
65 70 75 80

Gly Leu Leu Cys Ser Arg Ser Met Ser Gly Ile Ile Gln Pro Leu Thr
85 90 95

Ile Tyr Gly Pro Gln Gly Ile Arg Glu Phe Val Glu Thr Ala Leu Arg
100 105 110

Ile Ser Gly Ser Trp Thr Asp Tyr Pro Leu Glu Ile Val Glu Ile Gly
115 120 125

Ala Gly Glu Ile Leu Asp Asp Gly Leu Arg Lys Val Thr Ala Tyr Pro
130 135 140

Leu Glu His Pro Leu Glu Cys Tyr Gly Tyr Arg Ile Glu Glu His Asp
145 150 155 160

Lys Pro Gly Ala Leu Asn Ala Gln Ala Leu Lys Ala Ala Gly Val Pro
165 170 175

Pro Gly Pro Leu Phe Gln Glu Leu Lys Ala Gly Lys Thr Ile Thr Leu
180 185 190

Glu Asp Gly Arg Gln Ile Asn Gly Ala Asp Tyr Leu Ala Ala Pro Val
195 200 205

Pro Gly Lys Ala Leu Ala Ile Phe Gly Asp Thr Gly Pro Cys Asp Ala
210 215 220

Ala Leu Asp Leu Ala Lys Gly Val Asp Val Met Val His Glu Ala Thr
225 230 235 240

Leu Asp Ile Thr Met Glu Ala Lys Ala Asn Ser Arg Gly His Ser Ser
245 250 255

Thr Arg Gln Ala Ala Thr Leu Ala Arg Glu Ala Gly Val Gly Lys Leu
260 265 270

Ile Ile Thr His Val Ser Ser Arg Tyr Asp Asp Lys Gly Cys Gln His
275 280 285

Leu Leu Arg Glu Cys Arg Ser Ile Phe Pro Ala Thr Glu Leu Ala Asn
290 295 300

Asp Phe Thr Val Phe Asn Val
305 310

<210> 231

<211> 326

<212> PRT

<213> Synechocystis sp.

<400> 231

Met Glu Ile Thr Phe Leu Gly Thr Ser Ser Gly Val Pro Thr Arg Asn
1 5 10 15

Arg Asn Val Ser Ser Ile Ala Leu Arg Leu Pro Gln Arg Ala Glu Leu
20 25 30

Trp Leu Phe Asp Cys Gly Glu Gly Thr Gln His Gln Phe Leu Arg Ser
35 40 45

Glu Val Lys Ile Ser Gln Leu Thr Arg Ile Phe Ile Thr His Leu His
50 55 60

Gly Asp His Ile Phe Gly Leu Met Gly Leu Leu Ala Ser Ser Gly Leu
65 70 75 80

Ala Gly Ser Gly Gln Gly Ile Glu Ile Tyr Gly Pro Glu Gly Leu Gly
85 90 95

Asp Tyr Leu Glu Ala Cys Cys Arg Phe Ser Ser Thr His Leu Gly Lys
100 105 110

Arg Leu Lys Val His Thr Val Arg Glu Asn Gly Leu Ile Tyr Glu Asp
115 120 125

Lys Asp Phe Gln Val His Cys Gly Leu Leu Lys His Arg Ile Pro Ala
130 135 140

TTT 23333333

Tyr Gly Tyr Arg Val Glu Glu Lys Gln Arg Pro Gly Arg Phe Asn Val
 145 150 155 160
 Glu Gln Ala Glu Ala Leu Gly Ile Pro Phe Gly Pro Ile Tyr Gly Gln
 165 170 175
 Leu Lys Gln Gly Lys Thr Val Thr Leu Glu Asp Gly Arg Arg Ile Arg
 180 185 190
 Gly Gln Asp Leu Cys Glu Pro Pro Glu Pro Gly Arg Lys Phe Val Tyr
 195 200 205
 Cys Thr Asp Thr Val Phe Cys Glu Glu Ala Ile Ala Leu Ala Gln Glu
 210 215 220
 Ala Asp Leu Leu Val His Glu Ala Thr Phe Ala His Gln Asp Ala Gln
 225 230 235 240
 Leu Ala Phe Asp Arg Leu His Ser Thr Ser Thr Met Ala Ala Gln Val
 245 250 255
 Ala Leu Leu Ala Asn Val Lys Gln Leu Ile Met Thr His Phe Ser Pro
 260 265 270
 Arg Tyr Ala Pro Gly Asn Pro Leu Gln Leu Glu Asn Leu Leu Ala Glu
 275 280 285
 Ala Gln Ala Ile Phe Pro Asn Thr Arg Leu Ala Arg Asp Phe Leu Thr
 290 295 300
 Val Glu Ile Pro Arg Arg Thr Ala Asp Pro Ala Ile Ala Met Ser Thr
 305 310 315 320
 Pro Gln Ala Ser Pro Ala
 325

<210> 232

<211> 307

<212> PRT

<213> Methanobacterium thermoautotrophicum

<400> 232

Met Met Glu Val Thr Phe Leu Gly Thr Ser Ser Ala Val Pro Ser Lys
 1 5 10 15
 Asn Arg Asn His Thr Ser Ile Ala Leu Arg Ile Pro Gly Glu Ile Phe
 20 25 30
 Leu Phe Asp Cys Gly Glu Gly Thr Gln Arg Gln Met Ala Leu Ala Gly
 35 40 45
 Ile Ser Pro Met Lys Val Thr Arg Ile Phe Ile Thr His Leu His Gly
 50 55 60
 Asp His Ile Leu Gly Ile Pro Gly Met Ile Gln Ser Met Gly Phe Arg
 65 70 75 80
 Gly Arg Glu Glu Pro Leu Asp Ile Tyr Gly Pro Pro Gly Ile His Glu
 85 90 95
 Leu His Glu Cys Ile Met Lys Met Gly Tyr Phe Thr Leu Asp Phe Asp
 100 105 110

His Ala Thr Lys Ala Ile Tyr Arg Trp Leu Leu Ser Asp Tyr Val Lys
 100 105 110
 Val Ser Asn Ile Ser Ala Asp Asp Met Leu Tyr Thr Glu Thr Asp Leu
 115 120 125
 Glu Glu Ser Met Asp Lys Ile Glu Thr Ile Asn Phe His Glu Val Lys
 130 135 140
 Glu Val Ala Gly Ile Lys Phe Trp Cys Tyr His Ala Gly His Val Leu
 145 150 155 160
 Gly Ala Ala Met Phe Met Ile Glu Ile Ala Gly Val Lys Leu Leu Tyr
 165 170 175
 Thr Gly Asp Phe Ser Arg Gln Glu Asp Arg His Leu Met Ala Ala Glu
 180 185 190
 Ile Pro Asn Ile Lys Pro Asp Ile Leu Ile Ile Glu Ser Thr Tyr Gly
 195 200 205
 Thr His Ile His Glu Lys Arg Glu Glu Arg Glu Ala Arg Phe Cys Asn
 210 215 220
 Thr Val His Asp Ile Val Asn Arg Gly Gly Arg Gly Leu Ile Pro Val
 225 230 235 240
 Phe Ala Leu Gly Arg Ala Gln Glu Leu Leu Leu Ile Leu Asp Glu Tyr
 245 250 255
 Trp Gln Asn His Pro Glu Leu His Asp Ile Pro Ile Tyr Tyr Ala Ser
 260 265 270
 Ser Leu Ala Lys Lys Cys Met Ala Val Tyr Gln Thr Tyr Val Asn Ala
 275 280 285
 Met Asn Asp Lys Ile Arg Lys Gln Ile Asn Ile Asn Asn Pro Phe Val
 290 295 300
 Phe Lys His Ile Ser Asn Leu Lys Ser Met Asp His Phe Asp Asp Ile
 305 310 315 320
 Gly Pro Ser Val Val Met Ala Ser Pro Gly Met Met Gln Ser Gly Leu
 325 330 335
 Ser Arg Glu Leu Phe Glu Ser Trp Cys Thr Asp Lys Arg Asn Gly Val
 340 345 350
 Ile Ile Ala Gly Tyr Cys Val Glu Gly Thr Leu Ala Lys His Ile Met
 355 360 365
 Ser Glu Pro Glu Glu Ile Thr Thr Met Ser Gly Gln Lys Leu Pro Leu
 370 375 380
 Lys Met Ser Val Asp Tyr Ile Ser Phe Ser Ala His Thr Asp Tyr Gln
 385 390 395 400
 Gln Thr Ser Glu Phe Ile Arg Ala Leu Lys Pro Pro His Val Ile Leu
 405 410 415
 Val His Gly Glu Gln Asn Glu Met Ala Arg Leu Lys Ala Ala Leu Ile
 420 425 430

T002T = 29988560
 058863 1200

Arg Glu Tyr Glu Asp Asn Asp Glu Val His Ile Glu Val His Asn Pro
 435 440 445
 Arg Asn Thr Glu Ala Val Thr Leu Asn Phe Arg Gly Glu Lys Leu Ala
 450 455 460
 Lys Val Met Gly Phe Leu Ala Asp Lys Lys Pro Glu Gln Gly Gln Arg
 465 470 475 480
 Val Ser Gly Ile Leu Val Lys Arg Asn Phe Asn Tyr His Ile Leu Ser
 485 490 495
 Pro Cys Asp Leu Ser Asn Tyr Thr Asp Leu Ala Met Ser Thr Val Lys
 500 505 510
 Gln Thr Gln Ala Ile Pro Tyr Thr Gly Pro Phe Asn Leu Leu Cys Tyr
 515 520 525
 Gln Leu Gln Lys Leu Thr Gly Asp Val Glu Glu Leu Glu Ile Gln Glu
 530 535 540
 Lys Pro Ala Leu Lys Val Phe Lys Asn Ile Thr Val Ile Gln Glu Pro
 545 550 555 560
 Gly Met Val Val Leu Glu Trp Leu Ala Asn Pro Ser Asn Asp Met Tyr
 565 570 575
 Ala Asp Thr Val Thr Thr Val Ile Leu Glu Val Gln Ser Asn Pro Lys
 580 585 590
 Ile Arg Lys Gly Ala Val Gln Lys Val Ser Lys Lys Leu Glu Met His
 595 600 605
 Val Tyr Ser Lys Arg Leu Glu Ile Met Leu Gln Asp Ile Phe Gly Glu
 610 615 620
 Asp Cys Val Ser Val Lys Asp Asp Ser Ile Leu Ser Val Thr Val Asp
 625 630 635 640
 Gly Lys Thr Ala Asn Leu Asn Leu Glu Thr Arg Thr Val Glu Cys Glu
 645 650 655
 Glu Gly Ser Glu Asp Asp Glu Ser Leu Arg Glu Met Val Glu Leu Ala
 660 665 670
 Ala Gln Arg Leu Tyr Glu Ala Leu Thr Pro Val His
 675 680

<210> 234
 <211> 693
 <212> PRT
 <213> Arabidopsis thaliana

<400> 234
 Met Ala Ser Ser Ser Thr Ser Leu Lys Arg Arg Glu Gln Pro Ile Ser
 1 5 10 15
 Arg Asp Gly Asp Gln Leu Ile Val Thr Pro Leu Gly Ala Gly Ser Glu
 20 25 30
 Val Gly Arg Ser Cys Val Tyr Met Ser Phe Arg Gly Lys Asn Ile Leu
 35 40 45

Thr Leu Met Asn Gly Leu Thr Ala Pro Leu Asn Met Gln Val His Tyr
 385 390 395 400
 Ile Ser Phe Ser Ala His Ala Asp Tyr Ala Gln Thr Ser Thr Phe Leu
 405 410 415
 Lys Glu Leu Met Pro Pro Asn Ile Ile Leu Val His Gly Glu Ala Asn
 420 425 430
 Glu Met Met Arg Leu Lys Gln Lys Leu Leu Thr Glu Phe Pro Asp Gly
 435 440 445
 Asn Thr Lys Ile Met Thr Pro Lys Asn Cys Glu Ser Val Glu Met Tyr
 450 455 460
 Phe Asn Ser Glu Lys Leu Ala Lys Thr Ile Gly Arg Leu Ala Glu Lys
 465 470 475 480
 Thr Pro Asp Val Gly Asp Thr Val Ser Gly Ile Leu Val Lys Lys Gly
 485 490 495
 Phe Thr Tyr Gln Ile Met Ala Pro Asp Glu Leu His Val Phe Ser Gln
 500 505 510
 Leu Ser Thr Ala Thr Val Thr Gln Arg Ile Thr Ile Pro Phe Val Gly
 515 520 525
 Ala Phe Gly Val Ile Lys His Arg Leu Glu Lys Ile Phe Glu Ser Val
 530 535 540
 Glu Phe Ser Thr Asp Glu Glu Ser Gly Leu Pro Ala Leu Lys Val His
 545 550 555 560
 Glu Arg Val Thr Val Lys Gln Glu Ser Glu Lys His Ile Ser Leu Gln
 565 570 575
 Trp Ser Ser Asp Pro Ile Ser Asp Met Val Ser Asp Ser Ile Val Ala
 580 585 590
 Leu Ile Leu Asn Ile Ser Arg Glu Val Pro Lys Ile Val Met Glu Glu
 595 600 605
 Glu Asp Ala Val Lys Ser Glu Glu Glu Asn Gly Lys Lys Val Glu Lys
 610 615 620
 Val Ile Tyr Ala Leu Leu Val Ser Leu Phe Gly Asp Val Lys Leu Gly
 625 630 635 640
 Glu Asn Gly Lys Leu Val Ile Arg Val Asp Gly Asn Val Ala Gln Leu
 645 650 655
 Asp Lys Glu Ser Gly Glu Val Glu Ser Glu His Ser Gly Leu Lys Glu
 660 665 670
 Arg Val Arg Val Ala Phe Glu Arg Ile Gln Ser Ala Val Lys Pro Ile
 675 680 685
 Pro Leu Ser Ala Ser
 690

T0002T " 28988660

<211> 779

<212> PRT

<213> Saccharomyces cerevisiae

<400> 235

Met Glu Arg Thr Asn Thr Thr Thr Phe Lys Phe Phe Ser Leu Gly Gly
1 5 10 15

Ser Asn Glu Val Gly Arg Ser Cys His Ile Leu Gln Tyr Lys Gly Lys
20 25 30

Thr Val Met Leu Asp Ala Gly Ile His Pro Ala Tyr Gln Gly Leu Ala
35 40 45

Ser Leu Pro Phe Tyr Asp Glu Phe Asp Leu Ser Lys Val Asp Ile Leu
50 55 60

Leu Ile Ser His Phe His Leu Asp His Ala Ala Ser Leu Pro Tyr Val
65 70 75 80

Met Gln Arg Thr Asn Phe Gln Gly Arg Val Phe Met Thr His Pro Thr
85 90 95

Lys Ala Ile Tyr Arg Trp Leu Leu Arg Asp Phe Val Arg Val Thr Ser
100 105 110

Ile Gly Ser Ser Ser Ser Ser Met Gly Thr Lys Asp Glu Gly Leu Phe
115 120 125

Ser Asp Glu Asp Leu Val Asp Ser Phe Asp Lys Ile Glu Thr Val Asp
130 135 140

Tyr His Ser Thr Val Asp Val Asn Gly Ile Lys Phe Thr Ala Phe His
145 150 155 160

Ala Gly His Val Leu Gly Ala Ala Met Phe Gln Ile Glu Ile Ala Gly
165 170 175

Leu Arg Val Leu Phe Thr Gly Asp Tyr Ser Arg Glu Val Asp Arg His
180 185 190

Leu Asn Ser Ala Glu Val Pro Pro Leu Ser Ser Asn Val Leu Ile Val
195 200 205

Glu Ser Thr Phe Gly Thr Ala Thr His Glu Pro Arg Leu Asn Arg Glu
210 215 220

Arg Lys Leu Thr Gln Leu Ile His Ser Thr Val Met Arg Gly Gly Arg
225 230 235 240

Val Leu Leu Pro Val Phe Ala Leu Gly Arg Ala Gln Glu Ile Met Leu
245 250 255

Ile Leu Asp Glu Tyr Trp Ser Gln His Ala Asp Glu Leu Gly Gly Gly
260 265 270

Gln Val Pro Ile Phe Tyr Ala Ser Asn Leu Ala Lys Lys Cys Met Ser
275 280 285

Val Phe Gln Thr Tyr Val Asn Met Met Asn Asp Asp Ile Arg Lys Lys
290 295 300

Val Val Glu Trp Thr Gln Asp Leu Met Asn Asp Thr Val Ala Asp Ser
645 650 655

Ile Ile Ala Ile Leu Met Asn Val Asp Ser Ala Pro Ala Ser Val Lys
660 665 670

Leu Ser Ser His Ser Cys Asp Asp His Asp His Asn Asn Val Gln Ser
675 680 685

Asn Ala Gln Gly Lys Ile Asp Glu Val Glu Arg Val Lys Gln Ile Ser
690 695 700

Arg Leu Phe Lys Glu Gln Phe Gly Asp Cys Phe Thr Leu Phe Leu Asn
705 710 715 720

Lys Asp Glu Tyr Ala Ser Asn Lys Glu Glu Thr Ile Thr Gly Val Val
725 730 735

Thr Ile Gly Lys Ser Thr Ala Lys Ile Asp Phe Asn Asn Met Lys Ile
740 745 750

Leu Glu Cys Asn Ser Asn Pro Leu Lys Gly Arg Val Glu Ser Leu Leu
755 760 765

Asn Ile Gly Gly Asn Leu Val Thr Pro Leu Cys
770 775

<210> 236
 <211> 554
 <212> PRT
 <213> Synechocystis sp.

<400> 236
 Met Thr Phe Ser Val Pro Thr Gln Gly Lys Ala Phe Ala Asn Ile Ser
1 5 10 15

Phe Leu Pro Tyr Gly Val Gly Pro Arg Asp Gly Gly Ile Cys Leu Glu
20 25 30

Leu His Leu Gly Pro Tyr Arg Ile Leu Leu Asp Cys Gly Leu Glu Asp
35 40 45

Leu Thr Pro Leu Leu Ala Ala Asp Pro Gly Thr Val Asp Leu Val Phe
50 55 60

Cys Ser His Ala His Arg Asp His Gly Leu Gly Leu Trp Gln Phe His
65 70 75 80

Gln Gln Phe Pro His Ile Pro Ile Leu Ala Ser Glu Val Thr Gln Arg
85 90 95

Leu Leu Pro Leu Asn Trp Pro Asp Glu Phe Val Pro Pro Phe Cys Arg
100 105 110

Val Leu Pro Trp Arg Ser Pro Gln Glu Val Leu Pro Gly Leu Thr Val
115 120 125

Glu Leu Leu Pro Ala Gly His Leu Pro Gly Ala Ala Leu Ile Leu Leu
130 135 140

Glu Tyr His Asn Gly Asp Arg Leu Tyr Arg Val Ile Tyr Thr Gly Asp
145 150 155 160

Gln Arg Glu Leu Leu Lys Gln Asn Gln Ser Ser Lys Arg Pro Val Asp
 500 505 510

Phe Asp Cys Cys Ala Asn Cys Arg His Phe Gln His Tyr His Cys Arg
 515 520 525

Asn Pro Val Ser Pro Leu Met Gly Leu Glu Val Arg Ala Asp Gly His
 530 535 540

Cys Pro Val Phe Glu Ser Val Ala Ser Ser
 545 550

<210> 237
 <211> 636
 <212> PRT
 <213> Methanobacterium thermoautotrophicum

<400> 237
 Met Val Ser Glu Met Leu Glu Glu Ile Lys Arg Thr Ile Met Gln Arg
 1 5 10 15

Leu Pro Glu Arg Val Gln Val Ala Lys Val Glu Phe Glu Gly Pro Glu
 20 25 30

Val Val Ile Tyr Thr Lys Asn Pro Glu Ile Ile Thr Glu Asn Gly Asn
 35 40 45

Leu Ile Arg Asp Ile Ala Lys Asp Ile Arg Lys Arg Ile Ile Ile Arg
 50 55 60

Ser Asp Arg Ser Val Leu Met Asp Pro Glu Lys Ala Ile Arg Lys Ile
 65 70 75 80

His Glu Ile Val Pro Glu Glu Ala Lys Ile Thr Asn Ile Ser Phe Asp
 85 90 95

Asp Val Thr Cys Glu Val Ile Ile Glu Ala Arg Lys Pro Gly Leu Val
 100 105 110

Ile Gly Lys Tyr Gly Ser Thr Ser Arg Glu Ile Val Lys Asn Thr Gly
 115 120 125

Trp Ala Pro Lys Ile Leu Arg Thr Pro Pro Ile Ser Ser Glu Ile Ile
 130 135 140

Glu Arg Ile Arg Arg Thr Leu Arg Lys Asn Ser Lys Glu Arg Lys Lys
 145 150 155 160

Ile Leu Gln Gln Leu Gly Asn Arg Ile His Gln Lys Pro Lys Tyr Asp
 165 170 175

Asn Asp Trp Ala Arg Leu Thr Ala Met Gly Gly Phe Arg Glu Val Gly
 180 185 190

Arg Ser Cys Leu Tyr Leu Gln Thr Pro Asn Ser Arg Val Leu Leu Asp
 195 200 205

Cys Gly Val Asn Val Ala Gly Gly Asp Asp Lys Asn Ser Tyr Pro Tyr
 210 215 220

Leu Asn Val Pro Glu Phe Thr Leu Asp Ser Leu Asp Ala Val Ile Ile
 225 230 235 240

Thr His Ala His Leu Asp His Ser Gly Phe Leu Pro Tyr Leu Tyr His
 245 250 255
 Tyr Gly Tyr Asp Gly Pro Val Tyr Cys Thr Ala Pro Thr Arg Asp Leu
 260 265 270
 Met Thr Leu Leu Gln Leu Asp His Ile Asp Ile Ala His Arg Glu Asp
 275 280 285
 Glu Pro Leu Pro Phe Asn Val Lys His Val Lys Lys Ser Val Lys His
 290 295 300
 Thr Ile Thr Leu Asp Tyr Gly Glu Val Thr Asp Ile Ala Pro Asp Ile
 305 310 315 320
 Arg Leu Thr Leu His Asn Ala Gly His Ile Leu Gly Ser Ala Met Ala
 325 330 335
 His Leu His Ile Gly Asp Gly Gln His Asn Met Val Tyr Thr Gly Asp
 340 345 350
 Phe Lys Tyr Glu Gln Ser Arg Leu Leu Glu Ala Ala Ala Asn Arg Phe
 355 360 365
 Pro Arg Ile Glu Thr Leu Val Met Glu Ser Thr Tyr Gly Gly His Glu
 370 375 380
 Asp Val Gln Pro Ser Arg Asn Arg Ala Glu Lys Glu Leu Val Lys Thr
 385 390 395 400
 Ile Tyr Ser Thr Leu Arg Arg Gly Gly Lys Ile Leu Ile Pro Val Phe
 405 410 415
 Ala Val Gly Arg Ala Gln Glu Leu Met Ile Val Leu Glu Glu Tyr Ile
 420 425 430
 Arg Thr Gly Ile Ile Asp Glu Val Pro Val Tyr Ile Asp Gly Met Ile
 435 440 445
 Trp Glu Ala Asn Ala Ile His Thr Ala Arg Pro Glu Tyr Leu Ser Lys
 450 455 460
 Asp Leu Arg Asp Gln Ile Phe His Met Gly His Asn Pro Phe Ile Ser
 465 470 475 480
 Asp Ile Phe His Lys Val Asn Gly Met Asp Glu Arg Arg Glu Ile Val
 485 490 495
 Glu Gly Glu Pro Ser Ile Ile Leu Ser Thr Ser Gly Met Leu Thr Gly
 500 505 510
 Gly Asn Ser Leu Glu Tyr Phe Lys Trp Leu Cys Glu Asp Pro Asp Asn
 515 520 525
 Ser Leu Val Phe Val Gly Tyr Gln Ala Glu Gly Ser Leu Gly Arg Arg
 530 535 540
 Ile Gln Lys Gly Trp Lys Glu Ile Pro Leu Lys Asp Glu Asp Asp Lys
 545 550 555 560
 Met Arg Val Tyr Asn Val Arg Met Asn Ile Lys Thr Ile Glu Gly Phe
 565 570 575

0990667 1400
 T0007 2890660

Ser Gly His Ser Asp Arg Arg Gln Leu Met Glu Tyr Val Lys Arg Ile
 580 585 590

Ser Pro Lys Pro Glu Lys Ile Leu Leu Cys His Gly Asp Asn Tyr Lys
 595 600 605

Thr Leu Asp Leu Ala Ser Ser Ile Tyr Arg Thr Tyr Arg Ile Glu Thr
 610 615 620

Lys Thr Pro Leu Asn Leu Glu Thr Val Arg Ile Gln
 625 630 635

<210> 238
 <211> 1040
 <212> PRT
 <213> Homo sapiens

<400> 238
 Met Leu Glu Asp Ile Ser Glu Glu Asp Ile Trp Glu Tyr Lys Ser Lys
 1 5 10 15

Arg Lys Pro Lys Arg Val Asp Pro Asn Asn Gly Ser Lys Asn Ile Leu
 20 25 30

Lys Ser Val Glu Lys Ala Thr Asp Gly Lys Tyr Gln Ser Lys Arg Ser
 35 40 45

Arg Asn Arg Lys Arg Ala Ala Glu Ala Lys Glu Val Lys Asp His Glu
 50 55 60

Val Pro Leu Gly Asn Ala Gly Cys Gln Thr Ser Val Ala Ser Ser Gln
 65 70 75 80

Asn Ser Ser Cys Gly Asp Gly Ile Gln Gln Thr Gln Asp Lys Glu Thr
 85 90 95

Thr Pro Gly Lys Leu Cys Arg Thr Gln Lys Ser Gln His Val Ser Pro
 100 105 110

Lys Ile Arg Pro Val Tyr Asp Gly Tyr Cys Pro Asn Cys Gln Met Pro
 115 120 125

Phe Ser Ser Leu Ile Gly Gln Thr Pro Arg Trp His Val Phe Glu Cys
 130 135 140

Leu Asp Ser Pro Pro Arg Ser Glu Thr Glu Cys Pro Asp Gly Leu Leu
 145 150 155 160

Cys Thr Ser Thr Ile Pro Phe His Tyr Lys Arg Tyr Thr His Phe Leu
 165 170 175

Leu Ala Gln Ser Arg Ala Gly Asp His Pro Phe Ser Ser Pro Ser Pro
 180 185 190

Ala Ser Gly Gly Ser Phe Ser Glu Thr Lys Ser Gly Val Leu Cys Ser
 195 200 205

Leu Glu Glu Arg Trp Ser Ser Tyr Gln Asn Gln Thr Asp Asn Ser Val
 210 215 220

Ser Asn Asp Pro Leu Leu Met Thr Gln Tyr Phe Lys Lys Ser Pro Ser
 225 230 235 240

Leu	Thr	Glu	Ala	Ser 245	Glu	Lys	Ile	Ser	Thr	His	Ile	Gln	Thr	Ser	Gln
Gln	Ala	Leu	Gln 260	Phe	Thr	Asp	Phe	Val 265	Glu	Asn	Asp	Lys	Leu 270	Val	Gly
Val	Ala	Leu 275	Arg	Leu	Ala	Asn	Asn 280	Ser	Glu	His	Ile	Asn 285	Leu	Pro	Leu
Pro	Glu 290	Asn	Asp	Phe	Ser	Asp 295	Cys	Glu	Ile	Ser	Tyr 300	Ser	Pro	Leu	Gln
Ser 305	Asp	Glu	Asp	Thr	His 310	Asp	Ile	Asp	Glu	Lys 315	Pro	Asp	Asp	Ser	Gln 320
Glu	Gln	Leu	Phe	Phe 325	Thr	Glu	Ser	Ser	Lys 330	Asp	Gly	Ser	Leu 335	Glu	Glu
Asp	Asp	Asp	Ser 340	Cys	Gly	Phe	Phe	Lys 345	Lys	Arg	His	Gly	Pro 350	Leu	Leu
Lys	Asp	Gln 355	Asp	Glu	Ser	Cys	Pro 360	Lys	Val	Asn	Ser	Phe 365	Leu	Thr	Arg
Asp	Lys 370	Tyr	Asp	Glu	Gly	Leu 375	Tyr	Arg	Phe	Asn	Ser 380	Leu	Asn	Asp	Leu
Ser 385	Gln	Pro	Ile	Ser	Gln 390	Asn	Asn	Glu	Ser	Thr 395	Leu	Pro	Tyr	Asp	Leu 400
Ala	Cys	Thr	Gly	Gly 405	Asp	Phe	Val	Leu	Phe 410	Pro	Pro	Ala	Leu	Ala	Gly 415
Lys	Leu	Ala 420	Ala	Ser	Val	His	Gln 425	Ala	Thr	Lys	Ala	Lys	Pro 430	Asp	Glu
Pro	Glu	Phe 435	His	Ser	Ala	Gln	Ser 440	Asn	Lys	Gln	Lys	Gln 445	Val	Ile	Glu
Glu	Ser 450	Ser	Val	Tyr	Asn	Gln 455	Val	Ser	Leu	Pro	Leu 460	Val	Lys	Ser	Leu
Met 465	Leu	Lys	Pro	Phe	Glu 470	Ser	Gln	Val	Glu	Gly 475	Tyr	Leu	Ser	Ser	Gln 480
Pro	Thr	Gln	Asn	Thr 485	Ile	Arg	Lys	Leu	Ser 490	Ser	Glu	Asn	Leu	Asn	Ala 495
Lys	Asn	Asn	Thr 500	Asn	Ser	Ala	Cys	Phe 505	Cys	Arg	Lys	Ala	Leu 510	Glu	Gly
Val	Pro	Val 515	Gly	Lys	Ala	Thr	Ile 520	Leu	Asn	Thr	Glu	Asn 525	Leu	Ser	Ser
Thr	Pro 530	Ala	Pro	Lys	Tyr	Leu 535	Lys	Ile	Leu	Pro	Ser 540	Gly	Leu	Lys	Tyr
Asn 545	Ala	Arg	His	Pro	Ser 550	Thr	Lys	Val	Met	Lys 555	Gln	Met	Asp	Ile	Gly 560
Val	Tyr	Phe	Gly	Leu 565	Pro	Pro	Lys	Arg	Lys 570	Glu	Glu	Lys	Leu 575	Leu	Gly

Glu Ser Ala Leu Glu Gly Ile Asn Leu Asn Pro Val Pro Ser Pro Asn
 580 585 590
 Gln Lys Arg Ser Ser Gln Cys Lys Arg Lys Ala Glu Lys Ser Leu Ser
 595 600 605
 Asp Leu Glu Phe Asp Ala Ser Thr Leu His Glu Ser Gln Leu Ser Val
 610 615 620
 Glu Leu Ser Ser Glu Arg Ser Gln Arg Gln Lys Lys Arg Cys Arg Lys
 625 630 635 640
 Ser Asn Ser Leu Gln Glu Gly Ala Cys Gln Lys Arg Ser Asp His Leu
 645 650 655
 Ile Asn Thr Glu Ser Glu Ala Val Asn Leu Ser Lys Val Lys Val Phe
 660 665 670
 Thr Lys Ser Ala His Gly Gly Leu Gln Arg Gly Asn Lys Lys Ile Pro
 675 680 685
 Glu Ser Ser Asn Val Gly Gly Ser Arg Lys Lys Thr Cys Pro Phe Tyr
 690 695 700
 Lys Lys Ile Pro Gly Thr Gly Phe Thr Val Asp Ala Phe Gln Tyr Gly
 705 710 715 720
 Val Val Glu Gly Cys Thr Ala Tyr Phe Leu Thr His Phe His Ser Asp
 725 730 735
 His Tyr Ala Gly Leu Ser Lys His Phe Thr Phe Pro Val Tyr Cys Ser
 740 745 750
 Glu Ile Thr Gly Asn Leu Leu Lys Asn Lys Leu His Val Gln Glu Gln
 755 760 765
 Tyr Ile His Pro Leu Pro Leu Asp Thr Glu Cys Ile Val Asn Gly Val
 770 775 780
 Lys Val Val Leu Leu Asp Ala Asn His Cys Pro Gly Ala Val Met Ile
 785 790 795 800
 Leu Phe Tyr Leu Pro Asn Gly Thr Val Ile Leu His Thr Gly Asp Phe
 805 810 815
 Arg Ala Asp Pro Ser Met Glu Arg Ser Leu Leu Ala Asp Gln Lys Val
 820 825 830
 His Met Leu Tyr Leu Asp Thr Thr Tyr Cys Ser Pro Glu Tyr Thr Phe
 835 840 845
 Pro Ser Gln Gln Glu Val Ile Arg Phe Ala Ile Asn Thr Ala Phe Glu
 850 855 860
 Ala Val Thr Leu Asn Pro His Ala Leu Val Val Cys Gly Thr Tyr Ser
 865 870 875 880
 Ile Gly Lys Glu Lys Val Phe Leu Ala Ile Ala Asp Val Leu Gly Ser
 885 890 895
 Lys Val Gly Met Ser Gln Glu Lys Tyr Lys Thr Leu Gln Cys Leu Asn
 900 905 910

<400> 239																	
Met	Ser	Asn	Thr	Val	Glu	Asp	Asp	Asp	Asp	Asp	Phe	Gln	Ile	Pro	Pro		
1				5					10					15			
Ser	Ser	Gln	Leu	Ser	Ile	Arg	Lys	Pro	Leu	His	Pro	Thr	Asn	Ala	Asn		
			20					25					30				
Asn	Ile	Ser	His	Arg	Pro	Pro	Asn	Lys	Lys	Pro	Arg	Leu	Cys	Arg	Tyr		
		35					40					45					
Pro	Gly	Lys	Glu	Asn	Val	Thr	Pro	Pro	Pro	Ser	Pro	Asp	Pro	Asp	Leu		
	50					55					60						
Phe	Cys	Ser	Ser	Ser	Thr	Pro	His	Cys	Ile	Leu	Asp	Cys	Ile	Pro	Ser		
65					70					75					80		
Ser	Val	Asp	Cys	Ser	Leu	Gly	Asp	Phe	Asn	Gly	Pro	Ile	Ser	Ser	Leu		
				85					90					95			
Gly	Glu	Glu	Asp	Lys	Glu	Asp	Lys	Asp	Asp	Cys	Ile	Lys	Val	Asn	Arg		
			100					105					110				
Glu	Gly	Tyr	Leu	Cys	Asn	Ser	Met	Glu	Ala	Arg	Leu	Leu	Lys	Ser	Arg		
		115					120					125					
Ile	Cys	Leu	Gly	Phe	Asp	Ser	Gly	Ile	His	Glu	Asp	Asp	Glu	Gly	Phe		
	130					135					140						
Val	Glu	Ser	Asn	Ser	Glu	Leu	Asp	Val	Leu	Ile	Asn	Leu	Cys	Ser	Glu		
145					150					155							

